

(FILE 'HOME' ENTERED AT 18:03:27 ON 24 JAN 2007)

FILE 'BIOSIS' ENTERED AT 18:03:35 ON 24 JAN 2007

L1	2 S BURKHOLDERIA CASIDAE
L2	2 S CASIDAE
L3	3258 S BURKHOLDERIA
L4	3727 S PROBIOTIC
L5	1 S L3 AND L4
L6	89323 S PSEUDOMONAS
L7	41 S L6 AND L4
L8	2144 S PSEUDOMONAS CEPACIA
L9	0 S L8 AND L4
L10	74 S PSEUDOMONAS GLADIOLI
L11	0 S L10 AND L4
L12	492849 S ADMINISTR?
L13	4 S L12 AND L7
L14	483 S BURKHOLDERIA (P)DISEASE
L15	1 S BURKHOLDERIA (P)ANIMAL DISEASE
L16	9 S BURKHOLDERIA (P)GUT

**SCORE Search Results Details for Application
10776767 and Search Result
20070112_102005_us-10-776-767-1.rng.**

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10776767 and Search Result 20070112_102005_us-10-776-767-1.rnq.

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

```
Run on:      January 13, 2007, 13:59:11 ; Search time 1015 Seconds
              (without alignments)
              10269.469 Million cell updates/sec
```

Title: US-10-776-767-1
Perfect score: 1495
Sequence: 1 AAATATTACGCTGGTTGCAT.....TATCCGAAAGTTCGGCTGGA 1495

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

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Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query					ID	Description
	No.	Score	Match	Length	DB		
1	1493.4	99.9	1495	2	AAV34335	Aav34335	Burkholde
2	1364	91.2	1526	2	AAT01866	Aat01866	P.cepacia
3	1348.8	90.2	1535	2	AAV24295	Aav24295	Burkholde
4	1348.8	90.2	1535	10	ADB61689	Adb61689	16S rRNA
5	1312.6	87.8	1488	10	ADB61690	Adb61690	16S rRNA
6	1303	87.2	1610	10	ADB61691	Adb61691	16S rRNA
7	1293.4	86.5	1474	2	AAT18766	Aat18766	Pseudomon
8	1247.8	83.5	1343	15	AEF30349	Aef30349	Burkholde
9	1242.8	83.1	1477	2	AAX26285	Aax26285	16S rDNA
10	1192.6	79.8	1451	4	AAF74542	Aaf74542	Burkholde
11	1192.6	79.8	1451	10	ABX10819	Abx10819	Burkholde
12	1192.6	79.8	1451	12	ADH74483	Adh74483	TPA produ
13	1148.4	76.8	1532	2	AAQ26729	Aaq26729	16S rRNA
14	1148.4	76.8	1532	10	ADB61686	Adb61686	16S rRNA
15	1135.8	76.0	1485	10	ADB61687	Adb61687	16S rRNA
16	1135.6	76.0	1532	2	AAQ64008	Aaq64008	16S rRNA
17	1134.6	75.9	1496	12	ADQ16355	Adq16355	Nucleotid
18	1134.6	75.9	1496	14	AEA01071	Aea01071	Bordetell
19	1117.8	74.8	1453	6	ABL53376	Abl53376	Escherich
20	1117.8	74.8	1453	6	ABL53377	Abl53377	Escherich
21	1115.8	74.6	1400	8	ABZ69300	Abz69300	J lividum
22	1112.6	74.4	1387	3	AAA60564	Aaa60564	Vibrio sp
23	1112.6	74.4	1400	8	ABZ69299	Abz69299	J lividum
24	1111.4	74.3	1464	10	ADB61688	Adb61688	16S rRNA
25	1111	74.3	1400	8	ABZ69298	Abz69298	J lividum
26	1111	74.3	1452	2	AAX26375	Aax26375	16s rRNA
27	1110.6	74.3	1482	8	ABZ69304	Abz69304	Janthinob
28	1109.2	74.2	1400	8	ABZ69297	Abz69297	J lividum
29	1107.2	74.1	1481	10	ADE11077	Ade11077	Acidovora
30	1106.6	74.0	1509	12	ADQ67894	Adq67894	Acidovora
c 31	1104.6	73.9	1453	10	ADG44143	Adg44143	Unknown o
c 32	1104.6	73.9	1453	10	ADG17998	Adg17998	Unknown b
c 33	1104.6	73.9	1453	11	ADL27933	Adl27933	RA2 16S r
c 34	1104.6	73.9	1453	12	ADF47789	Adf47789	Unknown b
35	1101.8	73.7	1509	12	ADQ67895	Adq67895	Acidovora
36	1099	73.5	1530	14	ADW12666	Adw12666	Variovora
37	1098.6	73.5	1485	4	AAC86030	Aac86030	16s rDNA,
38	1097.2	73.4	1463	10	ADC53929	Adc53929	Phenyl hy
39	1096.8	73.4	1495	6	ABQ78660	Abq78660	Nucleotid
40	1090.8	73.0	1460	4	AAC86026	Aac86026	16s rDNA,
41	1090	72.9	1343	3	AAA73019	Aaa73019	Ralstonia
c 42	1089.4	72.9	1539	10	ADG44145	Adg44145	Unknown o
c 43	1089.4	72.9	1539	10	ADG18000	Adg18000	Unknown b
c 44	1089.4	72.9	1539	11	ADL27935	Adl27935	RA6 16S r
c 45	1089.4	72.9	1539	12	ADF47791	Adf47791	Unknown b

ALIGNMENTS

RESULT 1

AAV34335

ID AAV34335 standard; DNA; 1495 BP.

XX

AC AAV34335;

XX

DT 27-AUG-2003 (revised)

DT 01-MAR-1999 (first entry)

XX

DE Burkholderia casidae 16S rRNA gene.

XX

KW Burkholderia casidae; 16S rRNA gene; biological control; antimicrobial;
KW ss.

XX

OS Burkholderia.

XX

PN WO9848276-A1.

XX

PD 29-OCT-1998.

XX

PF 23-APR-1998; 98WO-US008148.

XX

PR 23-APR-1997; 97US-0044532P.

PR 22-APR-1998; 98US-00063898.

XX

PA (PENN-) PENN STATE RES FOUND.

PA (VIRG) VIRGINIA TECH INTELLECTUAL PROPERTIES.

XX

PI Casida LE, Falkinham JO, Cain CC;

XX

DR WPI; 1998-610004/51.

XX

PT New isolated Burkholderia casidae bacterium - used for producing anti-
PT microbial preparations active against bacteria, yeast, filamentous fungi,
PT protozoa and algae.

XX

PS Claim 67; Fig 1; 88pp; English.

XX

CC This is the nucleotide sequence of the 16S rRNA gene of Burkholderia
 CC casidae (Bc), a novel predator bacterium that has biocontrol activity
 CC against a broad range of microorganisms, particularly microbial
 CC pathogens. Bc appears to have 5 16S rRNA operons. The DNA sequenced was a
 CC PCR product of genomic DNA from Bc strain 2.2N (ATCC 55961), generated by
 CC primers 27f (see AAV34336) and 1522r (see AAV34338). A claimed new pure
 CC culture or suspension of Bc or its variant which exhibits biocontrol
 CC activity has: (a) a 16S rRNA gene comprising a sequence that is at least
 CC 97% similar to the 1495 bp sequence, and (b) a stated cellular fatty acid
 CC composition. Also claimed are: (1) a cell-free filtrate or cell fraction
 CC prepared from a pure culture or suspension as above; (2) an antimicrobial
 CC preparation comprising an alcohol extract of a cell, cyst, culture,
 CC suspension, cell-free filtrate or cell fraction of Bc; (3) a method for
 CC producing an antimicrobial preparation from Bc; and (4) a method for
 CC isolating Bc or variant on the basis of 16S rRNA sequence and cellular
 CC fatty acid composition. The pure cultures or suspensions can be used as
 CC biocontrol compositions for treating or preventing a disease of a plant
 CC (claimed) such as a disease caused by Alternaria, Aspergillus, Botrytis,
 CC Cercospora, Cercosporidium, Geotrichum, Mycosphaerella, Mucor,
 CC Penicillium, Phoma, Phytophthora, Plasmopora, Pseudopeziza, Puccinia,
 CC Pythium, Rhizoctonia, Rhizopus, Saccharomyces, Septoria, Sporothrix,
 CC Stemphylium, Trichophyton, Verticillium, Erwinia, Pseudomonas or
 CC Xanthomonas (claimed). The plants may be e.g. safflower, cotton, flax,
 CC oat, canola, poinsettia, chrysanthemum, corn, soybean, wheat, rice,

CC alfalfa, sorghum, peanut, tobacco, tomato, pepper, cucumber, lettuce,
 CC green bean, lima bean, pea, cantaloupe, musk melon, citrus fruit, grape,
 CC banana, geranium, azalea, rose, tulip, petunia, orchid, carnation, pine,
 CC yew or spruce (claimed). The compositions can also be used in the
 CC treatment of microbial diseases of animals, fish, humans and to control
 CC protozoan and algal growth in aquatic environments. (Updated on 27-AUG-
 CC 2003 to correct OS field.)

XX

SQ Sequence 1495 BP; 379 A; 342 C; 473 G; 301 T; 0 U; 0 Other;

Query Match 99.9%; Score 1493.4; DB 2; Length 1495;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1494; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	AAATATTACGCTGGTTGCATGCCTTACAGCATGCAAGTCGAACGGCAGCACGGGTGCTTG	60
Db	1	AAATATTACGCTGGTTGCATGCCTTACAGCATGCAAGTCGAACGGCAGCACGGGTGCTTG	60
Qy	61	CACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACAATGTCTGTAGTGGGG	120
Db	61	CACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACAATGTCTGTAGTGGGG	120
Qy	121	GATAGCCCGGCGAAAGCCGGATTAATACCGCATACGATCTACGGATGAAAGCGGGGGACC	180
Db	121	GATAGCCCGGCGAAAGCCGGATTAATACCGCATACGATCTACGGATGAAAGCGGGGGACC	180
Qy	181	TTCGGGCCTCGCGCTATAGGGTTGGCCGATGGCTGATTAGCTAGTTGGTGGGGTAAAGGC	240
Db	181	TTCGGGCCTCGCGCTATAGGGTTGGCCGATGGCTGATTAGCTAGTTGGTGGGGTAAAGGC	240
Qy	241	CTACCAAGGCGACGATCAGTAGTTGTCTGAGAGGACGACCAGCCACACTGGGACTGAGAC	300
Db	241	CTACCAAGGCGACGATCAGTAGTTGTCTGAGAGGACGACCAGCCACACTGGGACTGAGAC	300
Qy	301	ACGGCCCAGACTCTTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTG	360
Db	301	ACGGCCCAGACTCTTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTG	360
Qy	361	ATCCAGCAATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGGAA	420
Db	361	ATCCAGCAATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGGAA	420
Qy	421	AGAAATCCTTGGTTCTAATATAGCCGGGGGATGACGGTACCGGAAGAATAAGCACCGGCT	480
Db	421	AGAAATCCTTGGTTCTAATATAGCCGGGGGATGACGGTACCGGAAGAATAAGCACCGGCT	480
Qy	481	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTAATCGGAATTACTGGG	540
Db	481	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTAATCGGAATTACTGGG	540
Qy	541	CGTAAAGCGTGCGCAGGCGGTTTGCTAAGACCGATGTGAAATCCCCGGGCTCAACCTGGG	600
Db	541	CGTAAAGCGTGCGCAGGCGGTTTGCTAAGACCGATGTGAAATCCCCGGGCTCAACCTGGG	600
Qy	601	AACTGCATTGGTGA CTGGCAGGCTAGAGTATGGCAGAGGGGGGTAGAATTCCACGTGTAG	660
Db	601	AACTGCATTGGTGA CTGGCAGGCTAGAGTATGGCAGAGGGGGGTAGAATTCCACGTGTAG	660
Qy	661	CAGTGAAATGCGTAGAGATGTGGAAGAATACCGATGGCGAAGGCAGCCCCCTGGGCCAAT	720
Db	661	CAGTGAAATGCGTAGAGATGTGGAAGAATACCGATGGCGAAGGCAGCCCCCTGGGCCAAT	720

Qy	721	ACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCTTGGTAGTCCAC	780
Db	721	ACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCTTGGTAGTCCAC	780
Qy	781	GCCCTAAACGATGTCAACTAGTTGTTGGGGATTTCATTTCTTAGTAACGTAGCTAACGCG	840
Db	781	GCCCTAAACGATGTCAACTAGTTGTTGGGGATTTCATTTCTTAGTAACGTAGCTAACGCG	840
Qy	841	TGAAGTTGACCGCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGA	900
Db	841	TGAAGTTGACCGCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGA	900
Qy	901	CCCGCACAAAGCGGTGGATGATGTGGATTAAATTCGATGCAACGCGAAAAACCTTACCTACC	960
Db	901	CCCGCACAAAGCGGTGGATGATGTGGATTAAATTCGATGCAACGCGAAAAACCTTACCTACC	960
Qy	961	CTTGACATGGTCGGAATCCCGCTGAGAGGTGGGAGTGCTCGAAAGAGAACCGGCGCACAG	1020
Db	961	CTTGACATGGTCGGAATCCCGCTGAGAGGTGGGAGTGCTCGAAAGAGAACCGGCGCACAG	1020
Qy	1021	GTGCTGCATGGCTGTCGTCAGCTCGTGTGTCGTGAGATGTTGGGTAAAGTCCCGCAACGAGC	1080
Db	1021	GTGCTGCATGGCTGTCGTCAGCTCGTGTGTCGTGAGATGTTGGGTAAAGTCCCGCAACGAGC	1080
Qy	1081	GCAACCCTTGTCTTAGTTGCTACGCAAGAGCACTCTAAGGAGACTGCCGGTGACAAACC	1140
Db	1081	GCAACCCTTGTCTTAGTTGCTACGCAAGAGCACTCTAAGGAGACTGCCGGTGACAAACC	1140
Qy	1141	GGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTCACACGTCA	1200
Db	1141	GGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTCACACGTCA	1200
Qy	1201	TACAATGGTCGGAACAGAGGGTTGCCACCCGCGAAGGGGAGCTAATCCAGAAAACCGAT	1260
Db	1201	TACAATGGTCGGAACAGAGGGTTGCCACCCGCGAAGGGGAGCTAATCCAGAAAACCGAT	1260
Qy	1261	CGTAGTCCGGATTGCACTCTGCACCTCGAGTGCATGAAGCTGGAATCGCTAGTAATCGCG	1320
Db	1261	CGTAGTCCGGATTGCACTCTGCACCTCGAGTGCATGAAGCTGGAATCGCTAGTAATCGCG	1320
Qy	1321	GATCAGCATGCCGCGGTGAATACTTTCCCGGGTTTGTACACACCGCCCGTCACACCATG	1380
Db	1321	GATCAGCATGCCGCGGTGAATACTTTCCCGGGTTTGTACACACCGCCCGTCACACCATG	1380
Qy	1381	GGAGTGGGTTTTACCAGAAGTGGCTAGTCTAACCGCAAGGAAGAACGGTCCCCACGGTAG	1440
Db	1381	GGAGTGGGTTTTACCAGAAGTGGCTAGTCTAACCGCAAGGAAGAACGGTCCCCACGGTAG	1440
Qy	1441	GATTCATGACTGGGTGAAGTCGTAACAAGTAGCCGTATCCGAAAGTTCGGCTGGA	1495
Db	1441	GATTCATGACTGGGTGAAGTCGTAACAAGTAGCCGTATCCGAAAGTTCGGCTGGA	1495

RESULT 2

AAT01866

ID AAT01866 standard; DNA; 1526 BP.

XX

AC AAT01866;

XX

DT 16-OCT-2003 (revised)

```

DT 03-AUG-1999 (first entry)
XX
DE P.cepacia 16S rRNA gene sequence.
XX
KW 16S rRNA; KK01; primer; PCR; amplification; probe; hybridisation;
KW detection; diagnosis; ds.
XX
OS Burkholderia cepacia.
XX
PN JP07255486-A.
XX
PD 09-OCT-1995.
XX
PF 23-MAR-1994; 94JP-00051739.
XX
PR 23-MAR-1994; 94JP-00051739.
XX
PA (CANO ) CANON KK.
XX
DR WPI; 1995-378541/49.
XX
PT Pseudomonas cepacia KK01 strain 16S rRNA gene - also related probes and
PT primers, useful for specific detection of P.cepacia strain KK01.
XX
PS Claim 1; Page 21; 21pp; Japanese.
XX
CC This sequence represents the 16S rRNA gene of Pseudomonas cepacia strain
CC KK01. Fragments of the nucleic acid sequence (see AAT01872-T02316) are
CC useful as primers and probes for the specific detection of P.cepacia
CC strain KK01. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 1526 BP; 382 A; 352 C; 486 G; 306 T; 0 U; 0 Other;

Query Match          91.2%;  Score 1364;  DB 2;  Length 1526;
Best Local Similarity 97.8%;  Pred. No. 0;
Matches 1467;  Conservative 0;  Mismatches 25;  Indels 8;  Gaps 8;

```

[illegible]

Qy	360	GATCCAGCAATGCCGCGTGTGTGAAGAAGGCCCTTCGGGTTGTAAAGCACTTTTGTCCGGA	419
Db	377	GATCCAGCAATGCCGCGTGTGTGAAGAAGGCCCTTCGGGTTGTAAAGCACTTTTGTCCGGA	436
Qy	420	AAGAAATCCTTGGTTCTAATATAGCCGGGGGATGACGGTACCGGAAGAATAAGCACCGGC	479
Db	437	AAGAAATCCTTGGCTCTAATACAGTCGGGGGATGACGGTACCGGAAGAATAAGCACCGGC	496
Qy	480	TAACCTACGTGCCAGCAGCCGCGGTAAATACGTAGGGTGCGAGCGTTAATCGGAATTACTGG	539
Db	497	TAACCTACGTGCCAGCAGCCGCGGTAAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGG	556
Qy	540	GCGTAAAGCGTGCGCAGGCGGTTTGTCTAAGACCGATGTGAAATCCCCGGGCTCAACCTGG	599
Db	557	GCGTAAAGCGTGCGCAGGCGGTTTGTCTAAGACCGATGTGAAATCCCCGGGCTCAACCTGG	616
Qy	600	GAACCTGCATTGGTGACTGGCAGGCTAGAGTATGGCAGAGGGGGGTAGAATTCACGTGTA	659
Db	617	GAACCTGCATTGGTGACTGGCAAGCTAGAGTATGGCAGAGGGGGGTAGAATTCACGTGTA	676
Qy	660	GCAGTGAAATGCGTAGAGATGTGGAAGAATACCGATGGCGAAGGCAGCCCCCTGGGCCAA	719
Db	677	GCAGTGAAATGCGTAGAGATGTGGAAGAATACCGATGGCGAAGGCAGCCCCCTGGGCCAA	736
Qy	720	TACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA	779
Db	737	TACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA	796
Qy	780	CGCCCTAAACGATGTCAACTAGTTGTTGGGGATTCAATTCCTTAGTAACGTAGCTAACGC	839
Db	797	CGCCCTAAACGATGTCAACTAGTTGTTGGGGATTCAATTCCTTAGTAACGTAGCTAACGC	856
Qy	840	GTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGG	899
Db	857	GTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGG	916
Qy	900	ACCCGCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTAC	959
Db	917	ACCCGCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTAC	976
Qy	960	CCTTGACATGGTCGGAATCCCGCTGAGAGGTGGGAGTGCTCGAAAGAGAACC GGCGCACA	1019
Db	977	CCTTGACATGGTCGGAATCCTGCTGAGAGGTGGGAGTGCTCGAAAGAGAACC GGCGCACA	1036
Qy	1020	GGTGCTGCATGGCTGTCTGTGAGCTCGTGCTGAGATGTTGGGTTAAGTCCCGCAACGAG	1079
Db	1037	GGTGCTGCATGGCTGTCTGTGAGCTCGTGCTGAGATGTTGGGTTAAGTCCCGCAACGAG	1096
Qy	1080	CGCAACCCTTGTCTTAGTTGCTACGCAAGAGCACTCTAAGGAGACTGCCGGTGACAAAC	1139
Db	1097	CGCAACCCTTGTCTTAGTTGCTACGCAAGAGCACTCTAAGGAGACTGCCGGTGACAAAC	1156
Qy	1140	CGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGC-TCACACGT	1198
Db	1157	CGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACACGT	1216
Qy	1199	CATACAATGGTCGGAACAGAGGGTTGCC-ACCCGCGAAGGGGAGCTAATCCCAGAAAACC	1257
Db	1217	CATACAATGGTCGGAACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCCCAGAAAACC	1276
Qy	1258	GATCGTAGTCCGGATTGCACTCTGCACCTCGAGTGCATGAAGCTGGAATCGCTAGTAATC	1311


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      |||
Db      1277 GATCGTAGTCCGGATTGCACTCTGCAACTCGAGTGCATGAAGCTGGAATCGCTAGTAATC 1336
      |||
Qy      1318 GCGGATCAGCATGCCGCGGTGAATACTTTCCCGGGTTTTGTACACACCGCCCGTCACACC 1377
      |||
Db      1337 GCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTAACACACCGCCCGTCACACC 1396
      |||
Qy      1378 ATGGGAGTGGGTTTTACCAGAAGTGGCTAGTCTAACCGCAAGGAAGAACGGTCCCCACGG 1437
      |||
Db      1397 ATGGGAGTGGGTTTTACCAGAAGTGGCTAGTCTAACCGCAAGG-AGGACGGTCACCACGG 1455
      |||
Qy      1438 TAGGATTCATGACT-GGGTGAAGTCGTAACAA-GTAGCCGTATCCGAAAGTTGCGCTGGA 1495
      |||
Db      1456 TAGGATTCATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGCTGGA 1515

```

RESULT 3

AAV24295

ID AAV24295 standard; DNA; 1535 BP.

XX

AC AAV24295;

XX

DT 14-SEP-1998 (first entry)

XX

DE Burkholderia cepacia 16S ribosomal RNA gene.

XX

KW Antibacterial; antimycobacterial; oligonucleotide; infection; therapy;

KW ribosome binding site; Shine-Dalgarno; ribosomal RNA; cystic fibrosis;

KW tuberculosis; ss.

XX

OS Burkholderia cepacia.

XX

PN WO9814567-A2.

XX

PD 09-APR-1998.

XX

PF 30-SEP-1997; 97WO-US018094.

XX

PR 01-OCT-1996; 96US-0027729P.

XX

PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.

XX

PI Martin WJ, Wisniowski P;

XX

DR WPI; 1998-240079/21.

XX

PT Use of oligo:nucleotide(s) corresponding to bacterial 16S rRNA - for
PT inhibiting bacterial protein expression and treating bacterial infection.

XX

PS Claim 26; Page 62-63; 73pp; English.

XX

CC This polynucleotide comprises the 16S ribosomal RNA (rRNA) gene of
CC Burkholderia cepacia. The invention relates to methods and compositions
CC for the treatment of Gram-negative bacterial infections employing novel
CC oligonucleotides as antimicrobial agents. The oligonucleotides are
CC targeted to the Shine-Dalgarno (SD) region of prokaryotes to inhibit
CC bacterial expression and hence inhibit bacterial infection. They
CC preferably comprise 10-35 consecutive bases of the 3' end of a bacterial
CC 16S rRNA (see also AAV24291-94). An oligonucleotide may also include a
CC transport moiety and may have DNA phosphate modifications to increase
CC nuclease resistance, or may be formulated in a liposome. A claimed method

SQ Sequence 1535 BP; 385 A; 355 C; 488 G; 307 T; 0 U; 0 Other;

Qy	1	AAATATTACGCTGCTTGCATGCTTACAGCATGCAAGTCGAACGGCAGCACGGGTGCTTG	60
Db	27	AGATTGAACGCTGGCGGCATGCTTAACA-CATGCAAGTCGAACGGCAGCACGGGTGCTTG	85
Qy	61	CACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACAATGTCTGTAGTGGGG	120
Db	86	CACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAAC-ATGTCCTGTAGTGGGG	144
Qy	121	GATAGCCCGGCAGAAAGCCGGATTAATACCGCATAACGATCTACGGATGAAAGCGGGGGACC	180
Db	145	GATAGCCCGGCAGAAAGCCGGATTAATACCGCATAACGATCTACGGATGAAAGCGGGGGACC	204
Qy	181	TTCGGGCCTCGCGCTATAGGGTTGGCCGATGGCTGATTAGCTAGTTGGTGGGGTAAAGGC	240
Db	205	TTCGGGCCTCGCGCTATAGGGTTGG-CGATGGCTGATTAGCTAGTTGGTGGGGTAAAGGC	263
Qy	241	CTACCAAGGCGACGATCAGTAG-TTGTCTGAGAGGACGACCAGCCACACTGGGACTGAGA	299
Db	264	CTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGA	323
Qy	300	CACGGCCCAGACTCTTACGGGAGGCAGCAGTGGGGAATTTTGACAATGGGCGAAAGCCT	359
Db	324	CACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGACAATGGGCGAAAGCCT	383
Qy	360	GATCCAGCAATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGGA	419
Db	384	GATCCAGCAATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGGA	443
Qy	420	AAGAAATCCTTGGTTCTAATATAGCCGGGGGATGACGGTACCGGAAGAATAAGCACCGGC	479
Db	444	AAGAAATCCTTGGCTCTAATACAGTCGGGGGATGACGGTACCGGAAGAATAAGCACCGGC	503
Qy	480	TAACCTACGTGCCAGCAGCCGCGGTAAATACGTAGGGTGCGAGCGTTAATCGGAATTACTGG	539
Db	504	TAACCTACGTGCCAGCAGCCGCGGTAAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGG	563
Qy	540	GCGTAAAGCGTGCGCAGGCGGTTTGCTAAGACCGATGTGAAATCCCGGGCTCAACCTGG	599
Db	564	GCGTAAAGCGTGCGCAGGCGGTTTGCTAAGACCGATGTGAAATCCCGGGCTCAACCTGG	623
Qy	600	GAACCTGCATTGGTGACTGGCAGGCTAGAGTATGGCAGAGGGGGGTAGAATTCCACGTGTA	659
Db	624	GAACCTGCATTGGTGACTGGCAGGCTAGAGTATGGCAGAGGGGGGTAGAATTCCACGTGTA	683
Qy	660	GCAGTGAAATGCGTAGAGATGTGGAAGAATACCGATGGCGAAGGCAGCCCCCTGGGCCAA	719
Db	684	GCAGTGAAATGCGTAGAGATGTGGAAGAATACCGATGGCGAAGGCAGCCCCCTGGGCCAA	743

Qy	720	TACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA	779
Db	744	TACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA	803
Qy	780	CGCCCTAAACGATGTCAACTAGTTGTTGGGGATTCAATTCCTTAGTAACGTAGCTAACGC	839
Db	804	CGCCCTAAACGATGTCAACTAGTTGTTGGGGATTCAATTCCTTAGTAACGTAGCTAACGC	863
Qy	840	GTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGG	899
Db	864	GTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGG	923
Qy	900	ACCCGCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTAC	959
Db	924	ACCCGCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTAC	983
Qy	960	CCTTGACATGGTCGGAATCCCGCTGAGAGGTGGGAGTGCTCGAAAGAGAACC GGCGCACA	1019
Db	984	CCTTGACATGGTCGGAATCCTGCTGAGAGGTGGGAGTGCTCGAAAGAGAACC GGCGCACA	1043
Qy	1020	GGTGCTGCATGGCTGTTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAG	1079
Db	1044	GGTGCTGCATGGCTGTTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAG	1103
Qy	1080	CGCAACCCTTGTCCTTAGTTGCTACGCAAGAGCACTCTAAGGAGACTGCCGGTGACAAAC	1139
Db	1104	CGCAACCCTTGTCCTTAGTTGCTACGCAAGAGCACTCTAAGGAGACTGCCGGTGACAAAC	1163
Qy	1140	CGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGC - TCACACGT	1198
Db	1164	CGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACACGT	1223
Qy	1199	CATACAATGGTCGGAACAGAGGGTTGCC - ACCCGGAAGGGGAGCTAATCCCAGAAAACC	1257
Db	1224	CATACAATGGTCGGAACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCCCAGAAAACC	1283
Qy	1258	GATCGTAGTCCGGATTGCACTCTGCACCTCGAGTGCATGAAGCTGGAATCGCTAGTAATC	1317
Db	1284	CATCGTAGTCCGGATTGCACTCTGCACCTCGAGTGCATGAAGCTGGAATCGCTAGTAATC	1343
Qy	1318	GCGGATCAGCATGCCGCGGTGAATACTTCCCGGGTTTTGTACACACCGCCCGTCACACC	1377
Db	1344	GCGGATCAGCATGCCGCGGTGAATACTTCCCGGGCTTGTACACACCGCCCGTCACACC	1403
Qy	1378	ATGGGAGTGGGTTTTACAGAAGTGGCTAGTCTAACCGCAAGGAAGACGGTCCCCACGG	1437
Db	1404	ATGGGAGTGGGTTTTACAGAAGTGGCTAGTCTAACCGCAAGG - AGGACGGTCACCACGG	1462
Qy	1438	TAGGATTCATGACT - GGGTGAAGTCGTAACAA - GTAGCCGTATCCGAAAGTTCGGCTGGA	1495
Db	1463	TAGGATTCATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGCTGGA	1522

RESULT 4

ADB61689

ID ADB61689 standard; DNA; 1535 BP.

XX

AC ADB61689;

XX

DT 04-DEC-2003 (first entry)

XX

DE 16S rRNA of Burkholderia cepacia DNA sequence.
 XX
 KW enriching mRNA; high quality bacterial mRNA; bacterial gene expression;
 KW poly-A tail; mRNA purification; oligo-dT capture;
 KW prokaryote mRNA purification; bridging oligonucleotide; targeting region;
 KW capture oligonucleotide; prokaryotic 16S rRNA; prokaryotic 23S rRNA;
 KW eukaryotic 17S rRNA; eukaryotic 18S rRNA; eukaryotic 28S rRNA;
 KW 28S eukaryotic rRNA bridging oligonucleotide; ds.
 XX
 OS Burkholderia cepacia.
 XX
 PN WO2003054162-A2.
 XX
 PD 03-JUL-2003.
 XX
 PF 19-DEC-2002; 2002WO-US041014.
 XX
 PR 20-DEC-2001; 2001US-00029397.
 XX
 PA (AMBI-) AMBION INC.
 XX
 PI Murphy GL, Whitley JP;
 XX
 DR WPI; 2003-663255/62.
 XX
 PT Depleting or isolating targeted nucleic acids e.g. rRNA, involves using a
 PT bridging oligonucleotide comprising bridging region and a targeting
 PT region complementary to a targeted nucleic acid, and a capture
 PT oligonucleotide.
 XX
 PS Claim 4; Page 173-174; 208pp; English.
 XX
 CC This invention relates to a novel method for isolating, depleting or
 CC separating a targeted nucleic acid, such as rRNA, from a sample
 CC comprising targeted and non-targeted nucleic acids. It effects a way of
 CC enriching for non-targeted nucleic acids such as mRNAs. Isolating
 CC sufficient quantities of high quality bacterial mRNA is a demanding
 CC process which impedes analysis of bacterial gene expression in the
 CC presence of host cells. A small percentage of bacterial mRNAs may be poly
 CC -A tailed, but these are targeted for degradation and tend to be
 CC unstable. As a result, the commonly employed method for mRNA purification
 CC with eukaryotic cells, oligo-dT capture, is ineffective. The present
 CC invention provides an alternative, more suitable method for mRNA
 CC purification from prokaryotes. The method of the invention comprises the
 CC incubation of a sample with a bridging oligonucleotide (containing a
 CC targeting region) and subsequently incubating with a capture
 CC oligonucleotide allowing the isolation of the target from the sample. The
 CC method is useful for depleting or isolating targeted nucleic acid, for
 CC example rRNA such as prokaryotic 16S or prokaryotic 23S, eukaryotic 17S
 CC or 18S or eukaryotic 28S rRNA, from a sample. The rRNA sequence may
 CC comprise any one of 64 fully defined sequences as given in the
 CC specification. The present sequence is that of a DNA sequence which
 CC represents the sequence of 16S rRNA of Burkholderia cepacia related to
 CC the invention.
 XX
 SQ Sequence 1535 BP; 385 A; 355 C; 488 G; 307 T; 0 U; 0 Other;

Query Match 90.2%; Score 1348.8; DB 10; Length 1535;
 Best Local Similarity 97.6%; Pred. No. 0;
 Matches 1464; Conservative 0; Mismatches 27; Indels 9; Gaps 9;

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Qy	61	CACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACAATGTCTGTAGTGGGG	120
Db	86	CACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAAC-ATGTCCTGTAGTGGGG	144
Qy	121	GATAGCCCGGCGAAAGCCGGATTAATACCGCATACGATCTACGGATGAAAGCGGGGGACC	180
Db	145	GATAGCCCGGCGAAAGCCGGATTAATACCGCATACGATCTACGGATGAAAGCGGGGGACC	204
Qy	181	TTCGGGCCTCGCGCTATAGGGTTGGCCGATGGCTGATTAGCTAGTTGGTGGGGTAAAGGC	240
Db	205	TTCGGGCCTCGCGCTATAGGGTTGG-CGATGGCTGATTAGCTAGTTGGTGGGGTAAAGGC	263
Qy	241	CTACCAAGGCGACGATCAGTAG-TTGTCTGAGAGGACGACCAGCCACACTGGGACTGAGA	299
Db	264	CTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGA	323
Qy	300	CACGGCCCAGACTCTTACGGGAGG CAGCAGTGGGGAATTTTGACAATGGGCGAAAGCCT	359
Db	324	CACGGCCCAGACTCCTACGGGAGG CAGCAGTGGGGAATTTTGACAATGGGCGAAAGCCT	383
Qy	360	GATCCAGCAATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGGA	419
Db	384	GATCCAGCAATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGGA	443
Qy	420	AAGAAATCCTTGGTTCTAATATAGCCGGGGGATGACGGTACCGGAAGAATAAGCACCGGC	479
Db	444	AAGAAATCCTTGGTTCTAATACAGTCGGGGGATGACGGTACCGGAAGAATAAGCACCGGC	503
Qy	480	TAACTACGTGCCAGCAGCCGCGTAATACGTAGGGTGCGAGCGTTAATCGGAATTACTGG	539
Db	504	TAACTACGTGCCAGCAGCCGCGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGG	563
Qy	540	GCGTAAAGCGTGCGCAGGCGGTTTGCTAAGACCGATGTGAAATCCCCGGGCTCAACCTGG	599
Db	564	GCGTAAAGCGTGCGCAGGCGGTTTGCTAAGACCGATGTGAAATCCCCGGGCTCAACCTGG	623
Qy	600	GAAGTGCATTGGTGACTGGCAGGCTAGAGTATGGCAGAGGGGGGTAGAATTCCACGTGTA	659
Db	624	GAAGTGCATTGGTGACTGGCAGGCTAGAGTATGGCAGAGGGGGGTAGAATTCCACGTGTA	683
Qy	660	GCAGTGAAATGCGTAGAGATGTGGAAGAATACCGATGGCGAAGGCAGCCCCCTGGGCCAA	719
Db	684	GCAGTGAAATGCGTAGAGATGTGGAAGAATACCGATGGCGAAGGCAGCCCCCTGGGCCAA	743
Qy	720	TACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA	779
Db	744	TACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA	803
Qy	780	CGCCCTAAACGATGTCAACTAGTTGTTGGGGATTCAATTCCTTAGTAACGTAGCTAACGC	839
Db	804	CGCCCTAAACGATGTCAACTAGTTGTTGGGGATTCAATTCCTTAGTAACGTAGCTAACGC	863
Qy	840	GTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGG	899
Db	864	GTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGG	923
Qy	900	ACCCGCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTAC	959

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Db      924 ACCCGCACAGCGGTGGATGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTAC 983
      |||
Qy      960 CCTTGACATGGTCGGAATCCCGCTGAGAGGTGGGAGTGCTCGAAAGAGAACCGGCGCACA 1019
      |||
Db      984 CCTTGACATGGTCGGAATCCTGCTGAGAGGTGGGAGTGCTCGAAAGAGAACCGGCGCACA 1043
      |||
Qy      1020 GGTGCTGCATGGCTGTCGTCAGCTCGTGTCTGAGATGTTGGGTAAAGTCCCGCAACGAG 1079
      |||
Db      1044 GGTGCTGCATGGCTGTCGTCAGCTCGTGTCTGAGATGTTGGGTAAAGTCCCGCAACGAG 1103
      |||
Qy      1080 CGCAACCCTTGTCTTAGTTGCTACGCAAGAGCACTCTAAGGAGACTGCCGGTGACAAAC 1139
      |||
Db      1104 CGCAACCCTTGTCTTAGTTGCTACGCAAGAGCACTCTAAGGAGACTGCCGGTGACAAAC 1163
      |||
Qy      1140 CGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGC-TCACACGT 1198
      |||
Db      1164 CGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACACGT 1223
      |||
Qy      1199 CATACAATGGTCGGAACAGAGGGTTGCC-ACCGCGAAGGGGAGCTAATCCCAGAAAACC 1257
      |||
Db      1224 CATACAATGGTCGGAACAGAGGGTTGCCAACCGCGAGGGGAGCTAATCCCAGAAAACC 1283
      |||
Qy      1258 GATCGTAGTCCGGATTGCACTCTGCACCTCGAGTGCATGAAGCTGGAATCGCTAGTAATC 1317
      |||
Db      1284 CATCGTAGTCCGGATTGCACTCTGCAACTCGAGTGCATGAAGCTGGAATCGCTAGTAATC 1343
      |||
Qy      1318 GCGGATCAGCATGCCGCGGTGAATACTTTCCCGGGTTTTGTACACACCGCCCGTCACACC 1377
      |||
Db      1344 GCGGATCAGCATGCCGCGGTGAATACTTTCCCGGGTTCTGTACACACCGCCCGTCACACC 1403
      |||
Qy      1378 ATGGGAGTGGGTTTTACCAGAAAGTGGCTAGTCTAACCGCAAGGAAGAACGGTCCCCACGG 1437
      |||
Db      1404 ATGGGAGTGGGTTTTACCAGAAAGTGGCTAGTCTAACCGCAAGG-AGGACGGTCACCACGG 1462
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Qy      1438 TAGGATTCATGACT-GGGTGAAGTCGTAACAA-GTAGCCGTATCCGAAAGTTGGGCTGGA 1495
      |||
Db      1463 TAGGATTCATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGCTGGA 1522

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RESULT 5

ADB61690

ID ADB61690 standard; DNA; 1488 BP.

XX

AC ADB61690;

XX

DT 04-DEC-2003 (first entry)

XX

DE 16S rRNA of Burkholderia mallei DNA sequence.

XX

KW enriching mRNA; high quality bacterial mRNA; bacterial gene expression;

KW poly-A tail; mRNA purification; oligo-dT capture;

KW prokaryote mRNA purification; bridging oligonucleotide; targeting region;

KW capture oligonucleotide; prokaryotic 16S rRNA; prokaryotic 23S rRNA;

KW eukaryotic 17S rRNA; eukaryotic 18S rRNA; eukaryotic 28S rRNA;

KW 28S eukaryotic rRNA bridging oligonucleotide; ds.

XX

OS Burkholderia mallei.

XX

PN WO2003054162-A2.

XX

PD 03-JUL-2003.
 XX
 PF 19-DEC-2002; 2002WO-US041014.
 XX
 PR 20-DEC-2001; 2001US-00029397.
 XX
 PA (AMBI-) AMBION INC.
 XX
 PI Murphy GL, Whitley JP;
 XX
 DR WPI; 2003-663255/62.
 XX
 PT Depleting or isolating targeted nucleic acids e.g. rRNA, involves using a
 PT bridging oligonucleotide comprising bridging region and a targeting
 PT region complementary to a targeted nucleic acid, and a capture
 PT oligonucleotide.
 XX
 PS Claim 4; Page 174; 208pp; English.
 XX
 CC This invention relates to a novel method for isolating, depleting or
 CC separating a targeted nucleic acid, such as rRNA, from a sample
 CC comprising targeted and non-targeted nucleic acids. It effects a way of
 CC enriching for non-targeted nucleic acids such as mRNAs. Isolating
 CC sufficient quantities of high quality bacterial mRNA is a demanding
 CC process which impedes analysis of bacterial gene expression in the
 CC presence of host cells. A small percentage of bacterial mRNAs may be poly
 CC -A tailed, but these are targeted for degradation and tend to be
 CC unstable. As a result, the commonly employed method for mRNA purification
 CC with eukaryotic cells, oligo-dT capture, is ineffective. The present
 CC invention provides an alternative, more suitable method for mRNA
 CC purification from prokaryotes. The method of the invention comprises the
 CC incubation of a sample with a bridging oligonucleotide (containing a
 CC targeting region) and subsequently incubating with a capture
 CC oligonucleotide allowing the isolation of the target from the sample. The
 CC method is useful for depleting or isolating targeted nucleic acid, for
 CC example rRNA such as prokaryotic 16S or prokaryotic 23S, eukaryotic 17S
 CC or 18S or eukaryotic 28S rRNA, from a sample. The rRNA sequence may
 CC comprise any one of 64 fully defined sequences as given in the
 CC specification. The present sequence is that of a DNA sequence which
 CC represents the sequence of 16S rRNA of Burkholderia mallei related to the
 CC invention.
 XX
 SQ Sequence 1488 BP; 373 A; 344 C; 480 G; 291 T; 0 U; 0 Other;

Query Match 87.8%; Score 1312.6; DB 10; Length 1488;
 Best Local Similarity 96.4%; Pred. No. 0;
 Matches 1439; Conservative 0; Mismatches 44; Indels 10; Gaps 9;

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Qy      1 AAATATTACGCTGGTTGCATGCCTTACAGCATGCAAGTCGAACGGCAGCACGGGTGCTTG 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 AGATTGAACGCTGGCGGCATGCCTTACA-CATGCAAGTCGAACGGCAGCACGGG--CTTC 57

Qy     61 CACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACAATGTCCTGTAGTGGGG 120
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     58 GGCCTGGTGGCGAGTGGTGAACGGGTGAGTAATACATCGGAAC-ATGTCCTGTAGTGGGG 116

Qy    121 GATAGCCCGCGCAAAGCCGGATTAATACCGCATACGATCTACGGATGAAAGCGGGGGACC 180
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    117 GATAGCCCGCGCAAAGCCGGATTAATACCGCATACGATCTGAGGATGAAAGCGGGGGACC 176

Qy    181 TTCGGGCCTCGCGCTATAGGGTTGGCCGATGGCTGATTAGCTAGTTGGTGGGGTAAAGGC 240

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Db	237		CTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGACGACCAGCCCACTGGGACTGAGA	296
Qy	300		CACGGCCAGACTCTTACGGGAGG CAGCAGTGGGGAATTTTGACAATGGGCGAAAGCCT	359
Db	297		CACGGCCAGACTCCTACGGGAGG CAGCAGTGGGGAATTTTGACAATGGGCGCAAGCCT	356
Qy	360		GATCCAGCAATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGGA	419
Db	357		GATCCAGCAATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGGA	416
Qy	420		AAGAAATCCTTGGTTCTAATATAGCCGGGGATGACGGTACCGGAAGAATAAGCACCGGC	479
Db	417		AAGAAATCATTCTGGCTAATACCCGGAGTGGATGACGGTACCGGAAGAATAAGCACCGGC	476
Qy	480		TAAC TACGTGCCAGCAGCCGCGGT AATACGTAGGGTGCGAGCGTTAATCGGAATTACTGG	539
Db	477		TAAC TACGTGCCAGCAGCCGCGGT AATACGTAGGGTGCGAGCGTTAATTGGAATTACTGG	536
Qy	540		GCGTAAAGCGTGCGCAGGCGGTTTGCTAAGACCGATGTGAAATCCCGGGCTCAACCTGG	599
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Qy	600		GAACTGCATTGGTGACTGGCAGGCTAGAGTATGGCAGAGGGGGGTAGAATTCCACGTGTA	659
Db	597		GAACTGCATTGGTGACTGGCAGGCTAGAGTATGGCAGAGGGGGGTAGAATTCCACGTGTA	656
Qy	660		GCAGTGAAATGCGTAGAGATGTGGAAGAATACCGATGGCGAAGGCAGCCCCCTGGGCCAA	719
Db	657		GCAGTGAAATGCGTAGAGATGTGGAAGAATACCGATGGCGAAGGCAGCCCCCTGGGCCAA	716
Qy	720		TACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA	779
Db	717		TACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA	776
Qy	780		CGCCCTAAACGATGTCAACTAGTTGTTGGGGATTCAATTCCTTAGTAACGTAGCTAACGC	839
Db	777		CGCCCTAAACGATGTCAACTAGTTGTTGGGGATTCAATTCCTTAGTAACGTAGCTAACGC	836
Qy	840		GTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAACTCAAAGGAATTGACGGGG	899
Db	837		GTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAACTCAAAGGAATTGACGGGG	896
Qy	900		ACCCGCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTAC	959
Db	897		ACCCGCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTAC	956
Qy	960		CCTTGACATGGTCGGAATCCCGCTGAGAGGTGGGAGTGCTCGAAAGAGAACCGGCGCACA	1019
Db	957		CCTTGACATGGTCGGAAGCCCGATGAGAGTTGGGCGTGCTCGAAAGAGAACCGGCGCACA	1016
Qy	1020		GGTGCTGCATGGCTGTCTGT CAGCTCGTGTCTGAGATGTTGGGTTAAGTCCCGCAACGAG	1079
Db	1017		GGTGCTGCATGGCTGTCTGT CAGCTCGTGTCTGAGATGTTGGGTTAAGTCCCGCAACGAG	1076
Qy	1080		CGCAACCCTTGTCCTTAGTTGCTACGCAAGAGCACTCTAAGGAGACTGCCGGTGACAAAC	1139


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Db      1077 CGCAACCCTTGTCTTAGTTGCTACGCAAGAGCACTCTAAGGAGACTGCCGGTGACAAAC 1136
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Db      1137 CGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACACGT 1196
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Db      1257 GATCGTAGTCCGGATTGCACTCTGCAACTCGAGTGCATGAAGCTGGAATCGCTAGTAATC 1316
Qy      1318 GCGGATCAGCATGCCGCGGTGAATACTTTCCCGGGTTTTGTACACACCGCCCGTCACACC 1377
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Db      1377 ATGGGAGTGGGTTTTACCAGAAGTGGCTAGTCTAACCGCAAGG-AGGACGGTCACCACGG 1435
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RESULT 6

ADB61691

ID ADB61691 standard; DNA; 1610 BP.

XX

AC ADB61691;

XX

DT 04-DEC-2003 (first entry)

XX

DE 16S rRNA of Burkholderia pseudomallei DNA sequence.

XX

KW enriching mRNA; high quality bacterial mRNA; bacterial gene expression;
 KW poly-A tail; mRNA purification; oligo-dT capture;
 KW prokaryote mRNA purification; bridging oligonucleotide; targeting region;
 KW capture oligonucleotide; prokaryotic 16S rRNA; prokaryotic 23S rRNA;
 KW eukaryotic 17S rRNA; eukaryotic 18S rRNA; eukaryotic 28S rRNA;
 KW 28S eukaryotic rRNA bridging oligonucleotide; ds.

XX

OS Burkholderia pseudomallei.

XX

PN WO2003054162-A2.

XX

PD 03-JUL-2003.

XX

PF 19-DEC-2002; 2002WO-US041014.

XX

PR 20-DEC-2001; 2001US-00029397.

XX

PA (AMBI-) AMBION INC.

XX

PI Murphy GL, Whitley JP;

XX

DR WPI; 2003-663255/62.

XX

PT Depleting or isolating targeted nucleic acids e.g. rRNA, involves using a

•

SCORE Search Results Details for Application 10776767 and Search Result 20070112_102015_us-10-776-767-1.rnpm.

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OM nucleic - nucleic search, using sw model

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(without alignments)
10969.686 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 86534536 seqs, 29229259966 residues

Total number of hits satisfying chosen parameters: 173069072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1495	100.0	1495	77	US-60-044-532-1	Sequence 1, Appli
3	1348.8	90.2	1535	1	PCT-US02-41014-41	Sequence 41, Appl
4	1348.8	90.2	1535	18	US-08-923-030-12	Sequence 12, Appl
5	1348.8	90.2	1535	22	US-09-349-883-12	Sequence 12, Appl
6	1348.8	90.2	1535	39	US-10-029-397A-41	Sequence 41, Appl
7	1348.8	90.2	1535	39	US-10-029-397B-41	Sequence 41, Appl
8	1312.6	87.8	1488	1	PCT-US02-41014-42	Sequence 42, Appl
9	1312.6	87.8	1488	39	US-10-029-397A-42	Sequence 42, Appl
10	1312.6	87.8	1488	39	US-10-029-397B-42	Sequence 42, Appl
11	1303	87.2	1610	1	PCT-US02-41014-43	Sequence 43, Appl
12	1303	87.2	1610	39	US-10-029-397A-43	Sequence 43, Appl
13	1303	87.2	1610	39	US-10-029-397B-43	Sequence 43, Appl
14	1268.4	84.8	1522	70	US-11-198-242-2	Sequence 2, Appli
15	1192.6	79.8	1451	42	US-10-219-549-1	Sequence 1, Appli
16	1192.6	79.8	1451	77	US-60-091-645-1	Sequence 1, Appli
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18	1148.4	76.8	1532	39	US-10-029-397A-38	Sequence 38, Appl
19	1148.4	76.8	1532	39	US-10-029-397B-38	Sequence 38, Appl
20	1135.8	76.0	1485	1	PCT-US02-41014-39	Sequence 39, Appl
21	1135.8	76.0	1485	39	US-10-029-397A-39	Sequence 39, Appl
22	1135.8	76.0	1485	39	US-10-029-397B-39	Sequence 39, Appl
23	1134.6	75.9	1496	60	US-10-723-365B-32	Sequence 32, Appl
24	1111.4	74.3	1464	1	PCT-US02-41014-40	Sequence 40, Appl
25	1111.4	74.3	1464	39	US-10-029-397A-40	Sequence 40, Appl
26	1111.4	74.3	1464	39	US-10-029-397B-40	Sequence 40, Appl
27	1107.2	74.1	1481	1	PCT-US03-09618-1	Sequence 1, Appli
28	1107.2	74.1	1481	49	US-10-397-551-1	Sequence 1, Appli
29	1107.2	74.1	1481	69	US-11-112-257-1	Sequence 1, Appli
c 30	1104.6	73.9	1453	50	US-10-464-356-4	Sequence 4, Appli
c 31	1104.6	73.9	1453	50	US-10-464-709-4	Sequence 4, Appli
c 32	1104.6	73.9	1453	50	US-10-464-724-4	Sequence 4, Appli
c 33	1104.6	73.9	1453	78	US-60-171-140-4	Sequence 4, Appli
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37	1098.6	73.5	1485	41	US-10-168-337A-10	Sequence 10, Appl
38	1095	73.2	1452	15	US-08-642-229-2	Sequence 2, Appli
39	1095	73.2	1452	18	US-08-965-623-2	Sequence 2, Appli
40	1095	73.2	1526	70	US-11-198-242-1	Sequence 1, Appli
41	1090.8	73.0	1460	41	US-10-168-337A-6	Sequence 6, Appli

SCORE Search Results Details for Application 10776767 Result 20070112_102007_us-10-776-

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This page gives you Search Results detail for the Application 10776767 and Search Result 20070112_102007_us-10-776-
[start](#) | [next page](#)

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: January 13, 2007, 14:34:41 ; Search time 8795 Seconds
(without alignments)
10869.971 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	1370.4	91.7	110000	15	CP000152_03	Continuation (4 of
8	1368.8	91.6	1517	15	AY946010	AY946010 Burkholde
9	1368.8	91.6	1520	15	AY946011	AY946011 Burkholde
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37	1358.2	90.8	1488	15	AY741332	AY741332 Burkholde
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ALIGNMENTS

RESULT 1

AR178244

LOCUS AR178244 1495 bp DNA linear PAT 20-APR-2002

DEFINITION Sequence 1 from patent US 6319497.

ACCESSION AR178244

VERSION AR178244.1 GI:20219382
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 1495)
 AUTHORS Casida,L.Earl. Jr., Falkinham,J.Oliver. III and Cain,C.Christopher.
 TITLE Non-obligate predatory bacterium burkholderia casidaeand uses thereof
 JOURNAL Patent: US 6319497-A 1 20-NOV-2001;
 FEATURES Location/Qualifiers
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ORIGIN

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Qy	61	CACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACAATGTCCTGTAGTGGGG	120
Db	61	CACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACAATGTCCTGTAGTGGGG	120
Qy	121	GATAGCCCGGCGAAAGCCGGATTAATACCGCATACGATCTACGGATGAAAGCGGGGGACC	180
Db	121	GATAGCCCGGCGAAAGCCGGATTAATACCGCATACGATCTACGGATGAAAGCGGGGGACC	180
Qy	181	TTCGGGCCTCGCGCTATAGGGTTGGCCGATGGCTGATTAGCTAGTTGGTGGGGTAAAGGC	240
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Qy	301	ACGGCCCAGACTCTTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTG	360
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Db	961	 CTTGACATGGTCGGAATCCCGCTGAGAGGTGGGAGTGCTCGAAAGAGAACCGGCGCACAG	1020
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RESULT 2


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AR473471
LOCUS      AR473471                1495 bp    DNA        linear    PAT 20-FEB-2004
DEFINITION Sequence 1 from patent US 6689357.
ACCESSION  AR473471
VERSION    AR473471.1  GI:42708950
KEYWORDS
SOURCE     Unknown.
  ORGANISM Unknown.
           Unclassified.
REFERENCE  1  (bases 1 to 1495)
  AUTHORS  Casida,L.E. Jr., Falkinham,J.O. III and Cain,C.C.
  TITLE    Non-obligate predatory bacterium Burkholderia casidae and uses
           thereof
  JOURNAL  Patent: US 6689357-A 1 10-FEB-2004;
           Virginia Tech Intellectual Properties, Inc. and The Penn State
           Research Foundation; Blacksburg, VA
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Qy	61	CACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACAATGTCTGTAGTGGGG	120
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Qy	181	TTCGGGCCTCGCGCTATAGGGTTGGCCGATGGCTGATTAGCTAGTTGGTGGGGTAAAGGC	240
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Qy	481	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTAATCGGAATTACTGGG	540
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Qy	541	CGTAAAGCGTGCGCAGGCGGTTTGCTAAGACCGATGTGAAATCCCGGGGCTCAACCTGGG	600
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RESULT 3

AF226727

LOCUS AF226727 1495 bp DNA linear BCT 13-SEP-2000

DEFINITION Burkholderia sp. casida 16S ribosomal RNA gene, partial sequence.

ACCESSION AF226727

VERSION AF226727.1 GI:7107388

KEYWORDS

SOURCE Burkholderia sp. casida

ORGANISM Burkholderia sp. casida

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

Burkholderiaceae; Burkholderia.

REFERENCE 1 (bases 1 to 1495)

AUTHORS Cain,C.C., Henry,A.T., Waldo,R.H. III, Casida,L.J. Jr. and Falkinham,J.O. III.

TITLE Identification and characteristics of a novel Burkholderia strain with broad-spectrum antimicrobial activity

JOURNAL Appl. Environ. Microbiol. 66 (9), 4139-4141 (2000)

PUBMED 10966443

REFERENCE 2 (bases 1 to 1495)

AUTHORS Cain,C.C. and Falkinham,J.O. III.

TITLE Direct Submission

JOURNAL Submitted (19-JAN-2000) Biology, Virginia Tech, Fralin Biotechnology Center, Blacksburg, VA 24061-0346, USA

FEATURES Location/Qualifiers

source

1..1495

/organism="Burkholderia sp. casida"

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/db_xref="taxon:115546"

rRNA

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/product="16S ribosomal RNA"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 1495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	1021	GTGCTGCATGGCTGTGTCAGCTCGTGTGTCGAGATGTTGGGTAAAGTCCCGCAACGAGC	1080
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RESULT 4

BSP491304

LOCUS BSP491304 1523 bp DNA linear BCT 18-JUN-2003

DEFINITION Burkholderia sp. CEB01056 16S rRNA gene, strain CEB01056.

ACCESSION AJ491304

VERSION AJ491304.1 GI:31873152

KEYWORDS 16S ribosomal RNA; 16S rRNA gene.

SOURCE Burkholderia sp. CEB01056

ORGANISM Burkholderia sp. CEB01056

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.

REFERENCE 1

AUTHORS Ramisse,V., Balandreau,J., Thibault,F., Vidal,D., Vergnaud,G. and Normand,P.

TITLE DNA-DNA hybridization study of Burkholderia species using genomic DNA macro-array analysis coupled to reverse genome probing

JOURNAL Int. J. Syst. Evol. Microbiol. 53 (Pt 3), 739-746 (2003)

PUBMED 12807195

REFERENCE 2 (bases 1 to 1523)

AUTHORS Ramisse,V.

TITLE Direct Submission

JOURNAL Submitted (21-JUN-2002) Ramisse V., Microbiologie, Centre d'Etudes du Bouchet, BP3, 91710 Vert le Petit, FRANCE

FEATURES

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ORIGIN

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Best Local Similarity 98.3%; Pred. No. 5.9;
Matches 1474; Conservative 0; Mismatches 18; Indels 8; Gaps 8;
    
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**SCORE Search Results Details for Application
10776767 and Search Result
20070112 102010 us-10-776-767-1.rst.**

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10776767 and Search Result 20070112 102010 us-10-776-767-1.rst.

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OM nucleic - nucleic search, using sw model

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Run on:      January 13, 2007, 14:51:42 ; Search time 7704 Seconds
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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 6	587.4	39.3	793	13	DU370470	DU370470 109826819
c 7	580	38.8	1033	14	DU743187	DU743187 ASNC1602.
c 8	579	38.7	889	5	CK280527	CK280527 EST743249
c 9	576.4	38.6	716	11	AQ957363	AQ957363 LERAP36TR
c 10	575	38.5	884	5	CK280528	CK280528 EST743250
c 11	571.6	38.2	756	9	DN469396	DN469396 USDA-FP_1
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c 14	562.4	37.6	1031	11	BH656222	BH656222 BOMJZ86TF
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c 16	562	37.6	1051	11	BZ494182	BZ494182 BONHR54TR
c 17	558.2	37.3	746	11	AQ957362	AQ957362 LERAP36TF
c 18	557.2	37.3	787	8	CO159272	CO159272 FLD1_12_C
c 19	555.2	37.1	1016	11	BZ426201	BZ426201 BONDZ28TF
c 20	553.8	37.0	1077	11	BZ450751	BZ450751 BONBQ63TR
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c 24	550.4	36.8	1079	11	BH705272	BH705272 BOMKA47TF
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c 28	538.2	36.0	890	14	DU476594	DU476594 109841575
c 29	527	35.3	974	11	BZ440868	BZ440868 BONKT51TR
c 30	521.6	34.9	860	8	CN757363	CN757363 ID0AAA1CE
c 31	521	34.8	924	13	DU101928	DU101928 JBnY023N1
c 32	520.8	34.8	861	14	DU486180	DU486180 109842109
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c 34	518.8	34.7	861	14	DU486177	DU486177 109842109
c 35	518.6	34.7	810	14	DU477669	DU477669 109841577
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c 44	508.2	34.0	854	14	DU477664	DU477664 109841577
c 45	506.6	33.9	844	14	DU485186	DU485186 109842107

ALIGNMENTS

RESULT 1
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SCORE Search Results Details for Application 10776767 and Search Result 20070112_102013_us-10-776-767-1.rni.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

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(without alignments)
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 36	899.2	60.1	269223	3	US-09-596-002-41	Sequence 41, Appl
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ALIGNMENTS

RESULT 1

US-09-063-898-1

; Sequence 1, Application US/09063898

; Patent No. 6319497

; GENERAL INFORMATION:

; APPLICANT: Casida, Jr., Lester E.

SCORE Search Results Details for Application 10776767 and Search Result 20070112_102021_us-10-776-767-1.rnpbm.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

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OM nucleic - nucleic search, using sw model

Run on: January 13, 2007, 15:27:11 ; Search time 2057 Seconds
(without alignments)
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SUMMARIES

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	2	1495	100.0	1495	8	US-10-776-767-1	Sequence 1, Appli
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	4	1312.6	87.8	1488	7	US-10-029-397A-42	Sequence 42, Appl
	5	1303	87.2	1610	7	US-10-029-397A-43	Sequence 43, Appl
	6	1268.4	84.8	1522	16	US-11-198-242-2	Sequence 2, Appli
	7	1192.6	79.8	1451	7	US-10-219-549-1	Sequence 1, Appli
	8	1148.4	76.8	1532	7	US-10-029-397A-38	Sequence 38, Appl
	9	1135.8	76.0	1485	7	US-10-029-397A-39	Sequence 39, Appl
	10	1134.6	75.9	1496	10	US-10-723-365B-32	Sequence 32, Appl
	11	1111.4	74.3	1464	7	US-10-029-397A-40	Sequence 40, Appl
	12	1107.2	74.1	1481	7	US-10-397-551-1	Sequence 1, Appli
	13	1107.2	74.1	1481	13	US-11-112-257-1	Sequence 1, Appli
c	14	1104.6	73.9	1453	7	US-10-464-724-4	Sequence 4, Appli
c	15	1104.6	73.9	1453	7	US-10-464-356-4	Sequence 4, Appli
c	16	1104.6	73.9	1453	7	US-10-464-709-4	Sequence 4, Appli
	17	1099	73.5	1530	9	US-10-875-161-1	Sequence 1, Appli
	18	1098.6	73.5	1485	7	US-10-168-337A-10	Sequence 10, Appl
	19	1095	73.2	1526	16	US-11-198-242-1	Sequence 1, Appli
	20	1090.8	73.0	1460	7	US-10-168-337A-6	Sequence 6, Appli
c	21	1089.4	72.9	1539	7	US-10-464-724-6	Sequence 6, Appli
c	22	1089.4	72.9	1539	7	US-10-464-356-6	Sequence 6, Appli
c	23	1089.4	72.9	1539	7	US-10-464-709-6	Sequence 6, Appli
c	24	1083.8	72.5	1467	7	US-10-464-724-2	Sequence 2, Appli
c	25	1083.8	72.5	1467	7	US-10-464-356-2	Sequence 2, Appli
c	26	1083.8	72.5	1467	7	US-10-464-709-2	Sequence 2, Appli
	27	1083.2	72.5	1454	7	US-10-464-724-7	Sequence 7, Appli
	28	1083.2	72.5	1454	7	US-10-464-356-7	Sequence 7, Appli
	29	1083.2	72.5	1454	7	US-10-464-709-7	Sequence 7, Appli
	30	1082.4	72.4	1460	7	US-10-168-337A-4	Sequence 4, Appli
	31	1080.4	72.3	1458	8	US-10-659-948A-3	Sequence 3, Appli
	32	1080.4	72.3	1458	8	US-10-659-980A-3	Sequence 3, Appli
	33	1080.4	72.3	1458	8	US-10-659-983A-3	Sequence 3, Appli
	34	1078.4	72.1	1459	7	US-10-168-337A-8	Sequence 8, Appli
	35	1078	72.1	1478	7	US-10-168-337A-3	Sequence 3, Appli
	36	1077.8	72.1	1491	8	US-10-659-948A-20	Sequence 20, Appl
	37	1077.8	72.1	1491	8	US-10-659-980A-20	Sequence 20, Appl
	38	1077.8	72.1	1491	8	US-10-659-983A-20	Sequence 20, Appl
	39	1076.6	72.0	1405	11	US-10-515-311-5	Sequence 5, Appli
	40	1075.4	71.9	1426	7	US-10-168-337A-9	Sequence 9, Appli
	41	1072.8	71.8	1460	7	US-10-168-337A-2	Sequence 2, Appli
	42	1071.8	71.7	1460	7	US-10-168-337A-1	Sequence 1, Appli
	43	1060.8	71.0	1457	8	US-10-659-948A-1	Sequence 1, Appli
	44	1060.8	71.0	1457	8	US-10-659-980A-1	Sequence 1, Appli
	45	1060.8	71.0	1457	8	US-10-659-983A-1	Sequence 1, Appli

ALIGNMENTS